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☐ 1: DNA Res. 1998 Feb 28;5(1):1-9.

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Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrhagic Escherichia coli O157:H7 derived from Sakai outbreak.

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Makino K, Ishii K, Yasunaga T, Hattori M, Yokoyama K, Yutsudo CH, Kubota Y, Yamaichi Y, Iida T, Yamamoto K, Honda T, Han CG, Ohtsubo E, Kasamatsu M, Hayashi T, Kuhara S, Shinagawa

Department of Molecular Microbiology, Research Institute for Microbial Diseases, Osaka University, Suita, Japan.

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Enterohemorrhagic Escherichia coli (EHEC) O157:H7, derived from outbreak in Sakai city, Japan in 1996, possesses two kinds of plasmids: a 93-kb plasmid termed pO157, found in clinical EHEC isolates world-wide and a 3.3-kb plasmid termed pOSAK1, prevalent in EHEC strains isolated in Japan. Complete nucleotide sequences of both plasmids have been determined, and the putative functions of the encoded proteins and the cis-acting DNA sequences have been analyzed. pO157 shares strikingly similar genes and DNA sequences with F-factor and the transmissible drug-resistant plasmid R100 for DNA replication, copy number control, plasmid segregation, conjugative functions and stable maintenance in the host, although it is defective in DNA transfer by conjugation due to the truncation and deletion of the required genes and DNA sequences. In addition, it encodes several proteins implicated in EHEC pathogenicity such as an EHEC hemolysin (HlyA), a catalase-peroxidase (KatP), a serine protease (EspP) and type II secretion system. pOSAK1 possesses a ColE1-like replication system, and the DNA sequence is extremely similar to that of a drug-resistant plasmid, NTP16, derived from